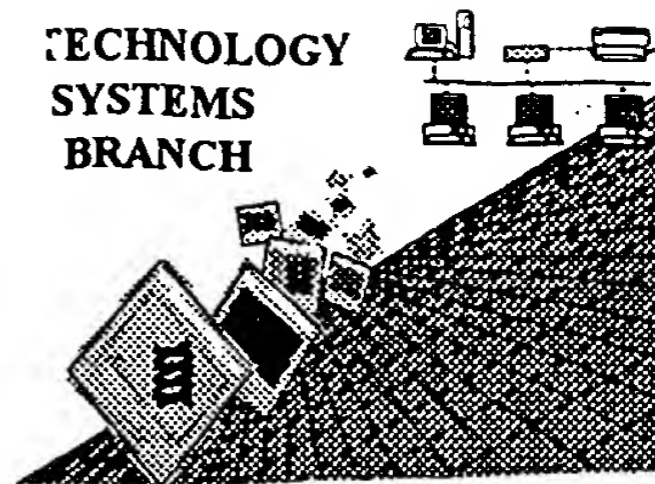O IPE

CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: _09/915,181_
Filing Date: _7/24/2001_
Date Processed by STIC: _1/26/2002_

STIC Contact: **Mark Spencer, 703-308-4212**

Nature of Problem:

The CRF (was):

✓ (circle one) Damaged or (Unreadable (for Unreadable, see attached)
___ Blank (no files on CRF) (see attached)
___ Empty file (filename present, but no bytes in file) (see attached)
___ Virus-infected. Virus name: _____ The STIC will not process the CRF.
___ Not saved in ASCII text
___ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.
___ Did not contain a Sequence Listing. (see attached sample)
___ Other:

**PLEASE USE THE CHECKER VERSION 3.1 PROGRAM TO REDUCE ERRORS.
SEE BELOW FOR ADDRESS:**
http:/www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio** (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
        Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service , or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

OIPE

RAW SEQUENCE LISTING   DATE: 04/08/2002
PATENT APPLICATION: US/09/915,181A   TIME: 15:33:00

Input Set : **A:\305-932610US.txt**
Output Set: **N:\CRF3\04082002\I915181A.raw**

ENTERED

```
 3 <110> APPLICANT: EDWARDS, ROBERT
 4        BELLOCCHIO, ELIZABETH
 5        FREMEAU, ROBERT
 6        REIMER, RICHARD
 8 <120> TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
10 <130> FILE REFERENCE: 305T-932610US
12 <140> CURRENT APPLICATION NUMBER: US 09/915,181A
13 <141> CURRENT FILING DATE: 2002-03-26
15 <150> PRIOR APPLICATION NUMBER: US 60/220,556
16 <151> PRIOR FILING DATE: 2000-07-25
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2607
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: misc_feature
29 <223> OTHER INFORMATION: n is a, g, c, or t
32 <400> SEQUENCE: 1
33 tgtgctctaa agcccccatt caaaatgcca tttaacgcat ttgatacctt caaagaaaaa    60
35 attttgaaac ccgggaagga aggagtgaag aatgccgtag gagattcgct ggggatctta   120
37 caaagaaaac tcgatgggac caacgaggag ggagatgcca ttgagctgag tgaggaagga   180
39 aggcctgtgc agacatccag agcccgagcc cctgtgtgcg actgcagctg ctgtggcatc   240
41 cccaagcggt acatcatcgc tgtcatgagt ggcctgggat tctgcatttc ctttgggatt   300
43 cggtgcaacc ttggagtggc cattgtggaa atggtcaaca atagcactgt gtatgtggat   360
45 gggaaaccgg aaatccagac agcacagttt aactgggatc cagagacggt gggaagggcg   420
47 aattctctta tccatggatc ttttttctgg ggttatattg tgacacaaat tcccggtggc   480
49 ttcatttcaa acaagtttgc tgctaacagg gtctttggag ctgccatctt cttgacgtca   540
51 accctgaaca tgttcatccc ttccgcggcc agggtgcatt acggctgtgt catgtgtgtg   600
53 aggattttgc agggtctggt ggagggtgtg acctacccag cctgccacgg gatgtggagt   660
55 aagtgggcac ctcccctgga gagaagtcgt ctagccacaa cctctttttg tggttcctat   720
57 gccggggcag tcgttgctat gcccccttgca ggagtattgg tgcagtacat tggctgggcc   780
59 tctgcctttt atatttacgg gatgtttgga attatttggt acatgttttg gctgctgctg   840
61 caggcttatg agtgtccagc agttcaccca acaatatcca atgaagaacg gacctacata   900
63 gagacaagta taggagaagg cgccaacttg gccagtctga gcaaattcaa cacaccatgg   960
65 agaaggtttt tcacatcctt gcctgtctat gccattattg tggcaaactt ttgtagaagc  1020
67 tggacccttct atttgctctt aataagtcag cctgcttact ttgaagaggt ctttgggttt  1080
69 gcaataagta aggtgggtct cttgtcagct gtcccacaca tggtgatgac aatcgtggta  1140
71 cccattggag acaactggc tgattattta agaagccgaa agatttttgac cacaactgct  1200
73 gtcagaaaga tcatgaattg tggaggcttt ggcatggagg caaccttgct cctggtggtt  1260
75 gggttttccc ataccaaagg agtggctatc tccttcctgg tgcttgctgt aggatttagt  1320
77 ggctttgcaa tttcaggttt caatgtcaac cacctggaca ttgctccacg atatgccagc  1380
```

```
 79 atcctcatgg ggatctcaaa tggcgtggga accctctctg gaatggtttg tcccctcatt   1440
 81 gttggtgcaa tgacaaagca caagacccgg gaagaatggc agaatgtgtt cctcatagca   1500
 83 gccctggtgc actacagtgg agtcatcttc tacggggtct ttgcttctgg ggaaaaacag   1560
 85 gactgggctg atccagagaa tctctctgag gagaaatgtg gaatcattga ccaagatgaa   1620
 87 ttagccgagg aaacagaact caaccacgag gctttcgtaa gtcccagaaa gaagatgtct   1680
 89 tatggagcca ccacccagaa ttgtgaggtc cagaagacgg atcggagaca acagagagaa   1740
 91 tccgccttcg aggggggagga gccattatcc taccagaatg aagaggactt ttcagaaaca   1800
 93 tcttaacgtg catcttcccc tcagcttaca accagaagtc tccacaccca ttgcttttcc   1860
 95 cataccttgg ccttccaggg ggccaaatca caggaaaggg ggagactaaa tcaacaacag   1920
 97 agaagaaaaa tgccttctta caaagatggg cgtatggatc ttggtctcag ttaattagat   1980
 99 agttgatcat attttttttg gggggggcaa ttgggcattg gctgttgagc cttctctcaa   2040
101 aagaacaatt tattcaggaa gaaatggcta gaagaataag gagtggcttg ttgctcaaat   2100
103 aaacactgaa gaaatccctc tttggtctgg agaagagtac atggtggttg ccaccccatc   2160
105 tccaaggata tccatgtaga ggacaatctc tgcaacctaa tgaagggaat cactcatggg   2220
107 ggcccttggt tgtgccaggt gctttatgaa cattcttatt taactcccac accctaatat   2280
109 agttattgta cccattttac aactaagaac attaaatgac taggttggcc cacccaaggt   2340
111 tgtcctctca gagccaaagc tgagactggc agatgaccag gagtttttagg aaggaaggaa   2400
113 ggaaggaagg aaggaaggaa ggaaggaagg aaggaaggaa ggaagggttc agttgagtgt   2460
115 agggtcattt tcaatgacaa aaacaaaaac tggaatcagt tggtttgtgg gtaattccat   2520
117 gtttggtcaa gggtgtgtgc atgcaaacgt gtatgtgcgt gtgtgtgtgt ttgtgtgttt   2580
119 gngtgtnagn nngnatnana anaaaan                                        2607
```

```
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 2607
124 <212> TYPE: DNA
125 <213> ORGANISM: Homo sapiens
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <223> OTHER INFORMATION: n is a, c, g, or t
132 <400> SEQUENCE: 2
```

```
133 acacgagatt tcgggggtaa gttttacggt aaattgcgta aactatggaa gtttcttttt     60
135 taaaactttg ggcccttcct tcctcacttc ttacggcatc ctctaagcga cccctagaat    120
137 gtttcttttg agctaccctg gttgctcctc cctctacggt aactcgactc actccttcct    180
139 tccggacacg tctgtaggtc tcgggctcgg ggacacacgc tgacgtcgac gacaccgtag    240
141 gggttcgcca tgtagtagcg acagtactca ccggaccata agacgtaaag gaaaccctaa    300
143 gccacgttgg aacctcaccg gtaacacctt taccagttgt tatcgtgaca catacaccta    360
145 ccctttggcc tttaggtctg tcgtgtcaaa ttgaccctag gtctctgcca cccttcccgc    420
147 ttaagagaat aggtacctag aaaaaagacc ccaatataac actgtgttta agggccaccg    480
149 aagtaaagtt tgttcaaacg acgattgtcc cagaaacctc gacggtagaa gaactgcagt    540
151 tgggacttgt acaagtaggg aaggcgccgg tcccacgtaa tgccgacaca gtacacacac    600
153 tcctaaaacg tcccagacca cctcccacac tggatgggtc ggacggtgcc ctacacctca    660
155 ttcacccgtg gaggggacct ctcttcagca gatcggtgtt ggagaaaaac accaaggata    720
157 cggccccgtc agcaacgata cggggaacgt cctcataacc acgtcatgta accgacccgg    780
159 agacggaaaa tataaatgcc ctacaaacct taataaacca tgtacaaaac cgacgacgac    840
161 gtccgaatac tcacaggtcg tcaagtgggt tgttataggt tacttcttgc ctggatgtat    900
163 ctctgttcat atcctcttcc gcggttgaac cggtcagact cgtttaagtt gtgtggtacc    960
165 tcttccaaaa agtgtaggaa cggacagata cggtaataac accgtttgaa aacatcttcg   1020
167 acctggaaga taaacgagaa ttattcagtc ggacgaatga aacttctcca gaaacccaaa   1080
169 cgttattcat tccacccaga gaacagtcga cagggtgtgt accactactg ttagcaccat   1140
171 gggtaacctc ctgttgaccg actaataaat tcttcggctt tctaaaactg gtgttgacga   1200
```

```
173 cagtctttct agtacttaac acctccgaaa ccgtacctcc gttggaacga ggaccaccaa 1260
175 cccaaaaggg tatggtttcc tcaccgatag aggaaggacc acgaacgaca tcctaaatca 1320
177 ccgaaacgtt aaagtccaaa gttacagttg gtggacctgt aacgaggtgc tatacggtcg 1380
179 taggagtacc cctagagttt accgcaccct tgggagagac cttaccaaac aggggagtaa 1440
181 caaccacgtt actgtttcgt gttctgggcc cttcttaccg tcttacacaa ggagtatcgt 1500
183 cgggaccacg tgatgtcacc tcagtagaag atgccccaga aacgaagacc ccttttttgtc 1560
185 ctgacccgac taggtctctt agagagactc ctctttacac cttagtaact ggttctactt 1620
187 aatcggctcc tttgtcttga gttggtgctc cgaaagcatt cagggtcttt cttctacaga 1680
189 atacctcggt ggtgggtctt aacactccag gtcttctgcc tagcctctgt tgtctctctt 1740
191 aggcggaagc tccccctcct cggtaatagg atggtcttac ttctcctgaa aagtctttgt 1800
193 agaattgcac gtagaagggg agtcgaatgt tggtcttcag aggtgtgggt aacgaaaagg 1860
195 gtatggaacc ggaaggtccc ccggtttagt gtcctttccc cctctgattt agttgttgtc 1920
197 tcttcttttt acggaagaat gtttctaccc gcatacctag aaccagagtc aattaatcta 1980
199 tcaactagta taaaaaaaac ccccccgtt aacccgtaac cgacaactcg gaagagagtt 2040
201 ttcttgttaa ataagtcctt ctttaccgat cttcttattc ctcaccgaac aacgagttta 2100
203 tttgtgactt ctttagggag aaaccagacc tcttctcatg taccaccaac ggtgggggtag 2160
205 aggttcctat aggtacatct cctgttagag acgttggatt acttccctta gtgagtaccc 2220
207 ccgggaacca acacggtcca cgaaatactt gtaagaataa attgagggtg tgggattata 2280
209 tcaataacat gggtaaaatg ttgattcttg taatttactg atccaaccgg gtgggttcca 2340
211 acaggagagt ctcggtttcg actctgaccg tctactggtc ctcaaaatcc ttccttcctt 2400
213 ccttccttcc ttccttcctt ccttccttcc ttccttcctt ccttcccaag tcaactcaca 2460
215 tcccagtaaa agttactgtt tttgttttg accttagtca accaaacacc cattaaggta 2520
217 caaaccagtt cccacacacg tacgtttgca catacacgca cacacacaca aacacacaaa 2580
219 cncacantcn nncntantnt tnttttn                                     2607
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 850
224 <212> TYPE: PRT
225 <213> ORGANISM: Homo sapiens
227 <400> SEQUENCE: 3
229 Cys Ala Leu Lys Pro Pro Phe Lys Met Pro Phe Asn Ala Phe Asp Thr
230 1               5                  10                  15
232 Phe Lys Glu Lys Ile Leu Lys Pro Gly Lys Glu Gly Val Lys Asn Ala
233            20                  25                  30
235 Val Gly Asp Ser Leu Gly Ile Leu Gln Arg Lys Leu Asp Gly Thr Asn
236            35                  40                  45
238 Glu Glu Gly Asp Ala Ile Glu Leu Ser Glu Glu Gly Arg Pro Val Gln
239        50                  55                  60
241 Thr Ser Arg Ala Arg Ala Pro Val Cys Asp Cys Ser Cys Cys Gly Ile
242 65                  70                  75                  80
244 Pro Lys Arg Tyr Ile Ile Ala Val Met Ser Gly Leu Gly Phe Cys Ile
245            85                  90                  95
247 Ser Phe Gly Ile Arg Cys Asn Leu Gly Val Ala Ile Val Glu Met Val
248            100                 105                 110
250 Asn Asn Ser Thr Val Tyr Val Asp Gly Lys Pro Glu Ile Gln Thr Ala
251            115                 120                 125
253 Gln Phe Asn Trp Asp Pro Glu Thr Val Gly Arg Ala Asn Ser Leu Ile
254        130                 135                 140
256 His Gly Ser Phe Phe Trp Gly Tyr Ile Val Thr Gln Ile Pro Gly Gly
257 145                 150                 155                 160
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/915,181A

DATE: 04/08/2002
TIME: 15:33:00

Input Set : A:\305-932610US.txt
Output Set: N:\CRF3\04082002\I915181A.raw

```
259 Phe Ile Ser Asn Lys Phe Ala Ala Asn Arg Val Phe Gly Ala Ala Ile
260               165             170             175
262 Phe Leu Thr Ser Thr Leu Asn Met Phe Ile Pro Ser Ala Ala Arg Val
263           180             185             190
265 His Tyr Gly Cys Val Met Cys Val Arg Ile Leu Gln Gly Leu Val Glu
266       195             200             205
268 Gly Val Thr Tyr Pro Ala Cys His Gly Met Trp Ser Lys Trp Ala Pro
269   210             215             220
271 Pro Leu Glu Arg Ser Arg Leu Ala Thr Thr Ser Phe Cys Gly Ser Tyr
272 225         230             235             240
274 Ala Gly Ala Val Val Ala Met Pro Leu Ala Gly Val Leu Val Gln Tyr
275           245             250             255
277 Ile Gly Trp Ala Ser Ala Phe Tyr Ile Tyr Gly Met Phe Gly Ile Ile
278       260             265             270
280 Trp Tyr Met Phe Trp Leu Leu Leu Gln Ala Tyr Glu Cys Pro Ala Val
281   275             280             285
283 His Pro Thr Ile Ser Asn Glu Glu Arg Thr Tyr Ile Glu Thr Ser Ile
284   290             295             300
286 Gly Glu Gly Ala Asn Leu Ala Ser Leu Ser Lys Phe Asn Thr Pro Trp
287 305         310             315             320
289 Arg Arg Phe Phe Thr Ser Leu Pro Val Tyr Ala Ile Ile Val Ala Asn
290           325             330             335
292 Phe Cys Arg Ser Trp Thr Phe Tyr Leu Leu Leu Ile Ser Gln Pro Ala
293       340             345             350
295 Tyr Phe Glu Glu Val Phe Gly Phe Ala Ile Ser Lys Val Gly Leu Leu
296   355             360             365
298 Ser Ala Val Pro His Met Val Met Thr Ile Val Val Pro Ile Gly Gly
299   370             375             380
301 Gln Leu Ala Asp Tyr Leu Arg Ser Arg Lys Ile Leu Thr Thr Thr Ala
302 385             390             395             400
304 Val Arg Lys Ile Met Asn Cys Gly Gly Phe Gly Met Glu Ala Thr Leu
305           405             410             415
307 Leu Leu Val Val Gly Phe Ser His Thr Lys Gly Val Ala Ile Ser Phe
308       420             425             430
310 Leu Val Leu Ala Val Gly Phe Ser Gly Phe Ala Ile Ser Gly Phe Asn
311       435             440             445
313 Val Asn His Leu Asp Ile Ala Pro Arg Tyr Ala Ser Ile Leu Met Gly
314   450             455             460
316 Ile Ser Asn Gly Val Gly Thr Leu Ser Gly Met Val Cys Pro Leu Ile
317 465             470             475             480
319 Val Gly Ala Met Thr Lys His Lys Thr Arg Glu Glu Trp Gln Asn Val
320           485             490             495
322 Phe Leu Ile Ala Ala Leu Val His Tyr Ser Gly Val Ile Phe Tyr Gly
323       500             505             510
325 Val Phe Ala Ser Gly Glu Lys Gln Asp Trp Ala Asp Pro Glu Asn Leu
326       515             520             525
328 Ser Glu Glu Lys Cys Gly Ile Ile Asp Gln Asp Glu Leu Ala Glu Glu
329   530             535             540
331 Thr Glu Leu Asn His Glu Ala Phe Val Ser Pro Arg Lys Lys Met Ser
```

file://C:\Crf3\Outhold\VsrI915181A.htm

4/8/02

```
332 545                    550                    555                    560
334 Tyr Gly Ala Thr Thr Gln Asn Cys Glu Val Gln Lys Thr Asp Arg Arg
335               565                    570                    575
337 Gln Gln Arg Glu Ser Ala Phe Glu Gly Glu Glu Pro Leu Ser Tyr Gln
338               580                    585                    590
340 Asn Glu Glu Asp Phe Ser Glu Thr Ser Arg Ala Ser Ser Pro Gln Leu
341               595                    600                    605
343 Thr Thr Arg Ser Leu His Thr His Cys Phe Ser His Thr Leu Ala Phe
344           610                    615                    620
346 Gln Gly Ala Lys Ser Gln Glu Arg Gly Arg Leu Asn Gln Gln Gln Arg
347 625                    630                    635                    640
349 Arg Lys Met Pro Ser Tyr Lys Asp Gly Arg Met Asp Leu Gly Leu Ser
350               645                    650                    655
352 Leu Asp Ser Ser Tyr Phe Phe Trp Gly Gly Gln Leu Gly Ile Gly Cys
353           660                    665                    670
355 Ala Phe Ser Gln Lys Asn Asn Leu Phe Arg Lys Lys Trp Leu Glu Glu
356           675                    680                    685
358 Gly Val Ala Cys Cys Ser Asn Lys His Arg Asn Pro Ser Leu Val Trp
359           690                    695                    700
361 Arg Arg Val His Gly Gly Cys His Pro Ile Ser Lys Asp Ile His Val
362 705                    710                    715                    720
364 Glu Asp Asn Leu Cys Asn Leu Met Lys Gly Ile Thr His Gly Gly Pro
365               725                    730                    735
367 Trp Leu Cys Gln Val Leu Tyr Glu His Ser Tyr Leu Thr Pro Thr Pro
368           740                    745                    750
370 Tyr Ser Tyr Cys Thr His Phe Thr Thr Lys Asn Ile Lys Leu Gly Trp
371           755                    760                    765
373 Pro Thr Gln Gly Cys Pro Leu Arg Ala Lys Ala Glu Thr Gly Arg Pro
374           770                    775                    780
376 Gly Val Leu Gly Arg Lys Glu Gly Arg Lys Glu Gly Arg Lys Glu Gly
377 785                    790                    795                    800
379 Arg Lys Glu Gly Arg Lys Gly Ser Val Glu Cys Arg Val Ile Phe Asn
380               805                    810                    815
382 Asp Lys Asn Lys Asn Trp Asn Gln Leu Val Cys Gly Phe His Val Trp
383           820                    825                    830
385 Ser Arg Val Cys Ala Cys Lys Arg Val Cys Ala Cys Val Cys Val Cys
386           835                    840                    845
388 Val Phe
389     850
391 <210> SEQ ID NO: 4
392 <211> LENGTH: 582
393 <212> TYPE: PRT
394 <213> ORGANISM: Rattus rattus
396 <400> SEQUENCE: 4
398 Met Glu Ser Val Lys Gln Arg Ile Leu Ala Pro Gly Lys Glu Gly Ile
399 1               5                    10                    15
401 Lys Asn Phe Ala Gly Lys Ser Leu Gly Gln Ile Tyr Arg Val Leu Glu
402           20                    25                    30
404 Lys Lys Gln Asp Asn Arg Glu Thr Ile Glu Leu Thr Glu Asp Gly Lys
```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/915,181A

DATE: 04/08/2002
TIME: 15:33:01

Input Set : A:\305-932610US.txt
Output Set: N:\CRF3\04082002\I915181A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2582,2587,2590,2591,2592,2594,2597,2599,2602,2607
Seq#:2; N Pos. 2582,2587,2590,2591,2592,2594,2597,2599,2602,2607
Seq#:9; N Pos. 1,2,3,5,9,10,11,12,13,14

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10,11